

Shin Lin Chen

1633

Errors Corrected by the STIC Systems Branch

Serial Number: 09/484, 964

CRF Processing Date: \_\_\_\_\_  
Edited by: \_\_\_\_\_  
Verified by: \_\_\_\_\_ (STIC sta: #9)

- ☐ Changed a file from non-ASCII to ASCII
- ☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.
- ☐ Edited a format error in the Current Application Data section, specifically: **ENTERED**
- ☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other \_\_\_\_\_
- ☐ Added the mandatory heading and subheadings for "Current Application Data".
- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: \_\_\_\_\_
- ☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: \_\_\_\_\_
- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: \_\_\_\_\_
- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- ☐ Inserted colons after headings/subheadings. Headings edited included: **RECEIVED**
- ☐ Deleted extra, invalid, headings used by an applicant, specifically: **JUN 25 2001**
- ☒ Deleted: ☒ non-ASCII "garbage" at the beginning/end of files; ☐ secretary's filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as \_\_\_\_\_
- ☐ Inserted mandatory headings, specifically: \_\_\_\_\_
- ☐ Corrected an obvious error in the response, specifically: \_\_\_\_\_
- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
- ☐ Corrected an error in the Number of Sequences field, specifically: \_\_\_\_\_
- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- ☐ Deleted *ending* stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: \_\_\_\_\_
- ☒ Other: Deleted extra bracket at <210> for seq. #12  
Added bracket to <210> for seq. #13

\*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form. 3/1/95

1633

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/484,964

DATE: 05/29/2001

TIME: 13:22:51

Input Set : A:\Cpg.pto

Output Set: C:\CRF3\05292001\I484964.raw

4 <110> APPLICANT: YEH, EDWARD T.H.  
6 <120> TITLE OF INVENTION: COMPOSITIONS AND USES FOR A NOVEL CELL-DEATH-PROTECTING  
7 PROTEIN  
10 <130> FILE REFERENCE: UTSH:248  
12 <140> CURRENT APPLICATION NUMBER: 09/484,964  
C--> 13 <141> CURRENT FILING DATE: 2000-01-18  
15 <150> PRIOR APPLICATION NUMBER: 08/964,162  
16 <151> PRIOR FILING DATE: 1997-11-04  
17 <150> PRIOR APPLICATION NUMBER: 60/030,302  
18 <151> PRIOR FILING DATE: 1996-11-05  
20 <160> NUMBER OF SEQ ID NOS: 16  
22 <170> SOFTWARE: PatentIn Ver. 2.0  
25 <210> SEQ ID NO: 1  
26 <211> LENGTH: 1465  
27 <212> TYPE: DNA  
28 <213> ORGANISM: Homo sapiens  
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31 <221> NAME/KEY: CDS  
32 <222> LOCATION: (88)..(390)  
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36 agacccccgg gtgaagccac cgtcatc 'atg tct gac cag gag gca aaa cct tca 114  
37 Met Ser Asp Gln Glu Ala Lys Pro Ser  
38 1 5  
39 act gag gac ttg ggg gat aag aag caa ggt gaa tat att aaa ctc aaa 162  
40 Thr Glu Asp Leu Gly Asp Lys Lys Gln Gly Glu Tyr Ile Lys Leu Lys  
41 10 15 20 25  
42 gtc att gga cag gat agc agt gag att cac ttc aaa gtg aaa atg aca 210  
43 Val Ile Gly Gln Asp Ser Ser Glu Ile His Phe Lys Val Lys Met Thr  
44 30 35 40  
45 aca cat ctc aag aaa ctc aaa gaa tca tac tgt caa aga cag ggt gtt 258  
46 Thr His Leu Lys Lys Leu Lys Glu Ser Tyr Cys Gln Arg Gln Gly Val  
47 45 50 55  
48 cca atg aat tca ctc agg ttt ctc ttt gag ggt cag aga att gct gat 306  
49 Pro Met Asn Ser Leu Arg Phe Leu Phe Glu Gly Gln Arg Ile Ala Asp  
50 60 65 70  
51 aat cat act cca aaa gaa ctg gga atg gag gaa gaa gat gtg att gaa 354  
52 Asn His Thr Pro Lys Glu Leu Gly Met Glu Glu Glu Asp Val Ile Glu  
53 75 80 85  
54 gtt tat cag gaa caa acg ggg ggt cat tca aca gtt tagatattct 400  
55 Val Tyr Gln Glu Gln Thr Gly Gly His Ser Thr Val  
56 90 95 100  
57 ttttattttt tttcttttcc ctcaatcctt ttttattttt aaaaatagtt cttttgtaat 460  
58 gtggtgttca aaacggaatt gaaaactggc accccatctc tttgaaacat ctggtaat 520  
59 gaattctagt gctcattatt cattattggt tgttttcatt gtgctgattt ttggtgatca 580  
60 agcctcagtc cccttcatat taccctctcc tttttaaaaa ttacgtgtgc acagagaggt 640  
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64 ctttccttaa cttgaagcta cttttaaaat ttgaggggtct ggaccaaag aagaggaata 880
65 tcaggttgaa gtcaagatga cagataaggt gagagtaatg actaactcca aagatggctt 940
66 cactgaagaa aaggcatttt aagatttttt aaaaatcttg tcagaagatc ccagaaaagt 1000
67 tctaattttc attagcaatt aataaagcta tacatgcaga aatgaatata acagaacact 1060
68 gctcttttta gattttattt gtactttttg gcctgggata tgggttttaa atggacattg 1120
69 tctgtaccag cttcattaaa ataaacaata tttgtcaaaa atcgtactaa tgcttatttt 1180
70 attttaattg tatagaaaga aaaaaatgcc taaaataagg ttttcttgca taaatactgg 1240
71 aaattgcaca tggtaacaaat tttttcttca ttactgtaca gggatgatgt taatgacttt 1300
72 ggagcactga aagttactga agtgccttct gaatcaagga ttaattaag gccacaatac 1360
73 ctttttaata ctcagtgttc tgtttttttt aaaaacttga tattcccgtg tgggtgcatat 1420
74 ttgatacagg tacccaatca tgttgataa atgggcatgc cagcc 1465

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76 &lt;210&gt; SEQ ID NO: 2

77 &lt;211&gt; LENGTH: 101

78 &lt;212&gt; TYPE: PRT

79 &lt;213&gt; ORGANISM: Homo sapiens

81 &lt;400&gt; SEQUENCE: 2

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82 Met Ser Asp Gln Glu Ala Lys Pro Ser Thr Glu Asp Leu Gly Asp Lys
83 1 5 10 15
84 Lys Gln Gly Glu Tyr Ile Lys Leu Lys Val Ile Gly Gln Asp Ser Ser
85 20 25 30
86 Glu Ile His Phe Lys Val Lys Met Thr Thr His Leu Lys Lys Leu Lys
87 35 40 45
88 Glu Ser Tyr Cys Gln Arg Gln Gly Val Pro Met Asn Ser Leu Arg Phe
89 50 55 60
90 Leu Phe Glu Gly Gln Arg Ile Ala Asp Asn His Thr Pro Lys Glu Leu
91 65 70 75 80
92 Gly Met Glu Glu Glu Asp Val Ile Glu Val Tyr Gln Glu Gln Thr Gly
93 85 90 95
94 Gly His Ser Thr Val
95 100

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97 &lt;210&gt; SEQ ID NO: 3

98 &lt;211&gt; LENGTH: 774

99 &lt;212&gt; TYPE: DNA

100 &lt;213&gt; ORGANISM: Homo sapiens

102 &lt;220&gt; FEATURE:

103 &lt;221&gt; NAME/KEY: modified\_base

104 &lt;222&gt; LOCATION: (53)

105 &lt;223&gt; OTHER INFORMATION: Y = C or T

W--&gt; 106 &lt;220&gt; FEATURE:

107 &lt;221&gt; NAME/KEY: modified\_base

108 &lt;222&gt; LOCATION: (689)

109 &lt;223&gt; OTHER INFORMATION: N = A, C, G or T

W--&gt; 110 &lt;220&gt; FEATURE:

111 &lt;221&gt; NAME/KEY: modified\_base

112 &lt;222&gt; LOCATION: (739)

113 &lt;223&gt; OTHER INFORMATION: N = A, C, G or T

W--&gt; 114 &lt;220&gt; FEATURE:

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117 <223> OTHER INFORMATION: N = A, C, G or T  
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121 gcggcagctg aggagactcc ggcgctcgcc atggccgacg aaaagcccaa ggaaggagtc 120  
122 aagactgaga acaacgatca tattaatttg aagggtggcg ggccaggatg ttctgtggtg 180  
123 cagtttaaga ttaagaggca tacaccactt agtaaaacta tgaaagccta ttgtgaacga 240  
124 cagggattgt caatgaggca gatcagattc cgatttgacg ggcaaccaat caatgaaaca 300  
125 gacacacctg cacagttgga aatggaggat gaagatacaa ttgatgtgtt ccaacagcag 360  
126 acgggaggtg tctactgaaa agggaaacctg cttctttact ccagaactct gttctttaaa 420  
127 gaccaagatt acatttctcaa ttagaaaact gcaatttggt tccaccacat cctgactact 480  
128 accgtatagt tttctctatt ctttcatttc ccccttcccc attcctttat tgtacataaa 540  
129 gtaactggta tatgtgcaca agcatattgc attttttttt tttttaacta aacagccaat 600  
130 ggtatgtttt gattgacatc caagtggaga cggggatggg gaaaaatact gattctgtgg 660  
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136 <212> TYPE: PRT  
137 <213> ORGANISM: Homo sapiens  
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142 His Ile Asn Leu Lys Val Ala Gly Gln Asp Gly Ser Val Val Gln Phe  
143 20 25 30  
144 Lys Ile Lys Arg His Thr Pro Leu Ser Lys Leu Met Lys Ala Tyr Cys  
145 35 40 45  
146 Glu Arg Gln Gly Leu Ser Met Arg Gln Ile Arg Phe Arg Phe Asp Gly  
147 50 55 60  
148 Gln Pro Ile Asn Glu Thr Asp Thr Pro Ala Gln Leu Glu Met Glu Asp  
149 65 70 75 80  
150 Glu Asp Thr Ile Asp Val Phe Gln Gln Gln Thr Gly Gly Val Tyr  
151 85 90 95

153 <210> SEQ ID NO: 5  
154 <211> LENGTH: 1733  
155 <212> TYPE: DNA  
156 <213> ORGANISM: Homo sapiens  
158 <220> FEATURE:  
159 <221> NAME/KEY: modified\_base  
160 <222> LOCATION: (19)  
161 <223> OTHER INFORMATION: N = A, C, G or T  
163 <400> SEQUENCE: 5

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166 tgtgaagaca gagaatgacc acatcaacct gaaggtggcc ggccaggacg gctccgtggt 180  
167 gcagttcaag atcaagaggc acacgtcgct gagcaagctg atgaaggcct actgcgagag 240  
168 gcagggcttg tcaatgaggc agatcagatt caggttcgac gggcagccaa tcaatgaaac 300  
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171 gcccggggccg tccatcctcg cattgctgtt gaatgggtgag cacgtgacca tgccgaccac 480
172 aaaggtgtct gcggaaactc gaggacattc accacgatga ttttcctctc tttgatgtac 540
173 ttcaagtgca actcaaaact atatctgcag ggatgaatct gtaacttaaa ttgggccaat 600
174 cagaattggt atctttgttc aggtaaaatg agttgcaaga tattgtgggt acttttgtgt 660
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176 atgttcgctt ttagtctggc cagggatctg actcctgagt tgggtgcctc tcccctgctc 780
177 actccagtc aatagagaat tgggttttcc cgcagtgagg attgcagctg ttggacaggt 840
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179 taaaatgcta aatattgcaa atttaagctt tgtcagtata tggaaaagtt gaagggaaaa 960
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181 gtgctctctg gccctcaagc atgtaacctc ggggtctgag gccagggacc cccccctg 1080
182 ccacccctcc caccctcctc cctgctcagt acctggcggt ggtacacagg caaggattgg 1140
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188 atttcagttc tgtgaaatat tttgggatct ataccaatta aacattttca tagttctgcc 1500
189 tattgtcctt ccctgaggct ccattgctgc ttggtggcca ttctctgcct tttacagtc 1560
190 acctgaacaa tgacccatca tctcttgctt gcttgaaatc ttgctgaaat gttctcattt 1620
191 cctgtttgct gtatgggctc ggggtgggatg tttgttggtc ctgttggtgt tattcaccaa 1680
192 tttgtacatt atttggtgtc ctttactact gtaaacagta aatatagttt ggt 1733

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194 <210> SEQ ID NO: 6

195 <211> LENGTH: 103

196 <212> TYPE: PRT

197 <213> ORGANISM: Homo sapiens

199 <400> SEQUENCE: 6

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202 Ile Asn Leu Lys Val Ala Gly Gln Asp Gly Ser Val Val Gln Phe Lys
203 20 25 30
204 Ile Lys Arg His Thr Ser Leu Ser Lys Leu Met Lys Ala Tyr Cys Glu
205 35 40 45
206 Arg Gln Gly Leu Ser Met Arg Gln Ile Arg Phe Arg Phe Asp Gly Glu
207 50 55 60
208 Pro Ile Asn Glu Thr Asp Thr Pro Ala Gln Leu Arg Met Glu Asp Glu
209 65 70 75 80
210 Asp Thr Ile Asp Val Phe Gln Gln Gln Thr Gly Gly Val Pro Glu Ser
211 85 90 95
212 Ser Leu Ala Gly His Ser Phe
213 100

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215 <210> SEQ ID NO: 7

216 <211> LENGTH: 9

217 <212> TYPE: PRT

218 <213> ORGANISM: Artificial Sequence

220 <220> FEATURE:

221 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic

222 Peptide

## RAW SEQUENCE LISTING

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229 <211> LENGTH: 30
230 <212> TYPE: DNA
231 <213> ORGANISM: Homo sapiens
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236 <210> SEQ ID NO: 9
237 <211> LENGTH: 30
238 <212> TYPE: DNA
239 <213> ORGANISM: Homo sapiens
241 <400> SEQUENCE: 9
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245 <210> SEQ ID NO: 10
246 <211> LENGTH: 7
247 <212> TYPE: PRT
248 <213> ORGANISM: Artificial Sequence
250 <220> FEATURE:
251 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
252     Peptide
254 <400> SEQUENCE: 10
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256   1                               5
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259 <211> LENGTH: 9
260 <212> TYPE: PRT
261 <213> ORGANISM: Influenza virus
263 <400> SEQUENCE: 11
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265   1                               5
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268 <211> LENGTH: 4
269 <212> TYPE: PRT
270 <213> ORGANISM: Homo sapiens
272 <400> SEQUENCE: 12
273 His Ser Thr Val
274   1
276 <210> SEQ ID NO: 13
277 <211> LENGTH: 101
278 <212> TYPE: PRT
279 <213> ORGANISM: Saccharomyces cerevisiae
281 <400> SEQUENCE: 13
282 Met Ser Asp Ser Glu Val Asn Gln Glu Ala Lys Pro Glu Val Lys Pro
283   1                               5                               10                               15
284 Glu Val Lys Pro Glu Thr His Ile Asn Leu Lys Val Ser Asp Gly Ser
285                               20                               25                               30
286 Ser Glu Ile Phe Phe Lys Ile Lys Lys Thr Thr Pro Leu Arg Arg Leu

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## VERIFICATION SUMMARY

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Output Set: C:\CRF3\05292001\I484964.raw

L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:106 M:283 W: Missing Blank Line separator, <220> field identifier  
L:110 M:283 W: Missing Blank Line separator, <220> field identifier  
L:114 M:283 W: Missing Blank Line separator, <220> field identifier  
L:131 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3  
L:132 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3  
L:164 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5